

PUBLICACIONES

- Brodie, J., et al. (2016) Characterising the microbiome of *Corallina officinalis*, a dominant calcified intertidal red alga. FEMS Microbiology Ecology. doi: 10.1093/femsec/fiw110.
- Campana, M. G., et al. (2014) False positives complicate ancient pathogen identifications using high-throughput shotgun sequencing. BMC Research Notes. 7:111 <http://www.biomedcentral.com/1756-0500/7/111>.
- Campella, M. A., et al. (2015) Genome expansion via lineage splitting and genome reduction in the cicada endosymbiont *Hodgkinia*. PNAS. doi: 10.1073/pnas.1421386112.
- Cervera-Juanes, R., et al. (2015) MAOA expression predicts vulnerability for alcohol use. Molecular Psychiatry. doi:10.1038/mp.2015.93.
- Chwialkowska, K., Nowakowska, U., Mrozievicz, A., Szarejko, I., and Kwasniewski, M. (2016) Water-deficiency conditions differently modulate the methylome of roots and leaves in barley (*Hordeum vulgare L.*) J. Exp. Bio. doi: 10.1093/jxb/erv552.
- Devall, M., et al. (2015) A comparison of mitochondrial DNA isolation methods in frozen post-mortem human brain tissue—applications for studies of mitochondrial genetics in brain disorders. Biotechniques 59(4): 241-246.
- DeWitt, M., Magis, W., Bray, N. et al. (2016, Jan 15). Efficient Correction of the Sickle Mutation in Human Hematopoietic Stem Cells Using a Cas9 Ribonucleoprotein Complex Retrieved from <http://biorxiv.org/content/early/2016/01/15/036236>
- doi: 10.1101/036236
- Gal, C., et al. (2015) Abo1, a conserved bromodomain AAA-ATPase, maintains global nucleosome occupancy and organization. EMBO Reports. 16:11. pp 1409 – 1580. doi: 10.15252/embr.201540476.
- Gal, C. et. al. (2015) The impact of the HIRA histone chaperone upon global nucleosome architecture. Cell Cycle. 14:1, 123-134. doi:10.4161/15384101.2014.967123.
- Gan, H. M., Tan, M. H., Lee, Y. P. and Austin, C. M. (2014) The complete mitogenome of the Australian tadpole shrimp *Triops australiensis* (Spencer & Hall, 1895) (Crustacea: Branchiopoda: Notostraca).
- Gan, H. M., Tan, M. H., Lee, Y. P. and Austin, C. M. (2014) The complete mitogenome of the river blackfish, *Gadopsis marmoratus* (Richardson, 1848) (Teleostei: Percichthyidae). Mitochondrial DNA. doi:10.3109/19401736.2014.974174.
- Givnish, T. J., et al. (2016) Phylogenomics and historical biogeography of the monocot order Liliales: out of Australia and through Antarctica. Cladistics. doi: 10.1111/cla.12153.
- Goh, H. F. and Philip, K. (2015) Purification and Characterization of Bacteriocin Produced by *Weissella confusa* A3 of Dairy Origin. PLoS ONE. doi: 10.1371/journal.pone.0140434.

- Gultekin, S. E., et al. (2016) Unusual Presentation of an Adenocarcinoma of the Lung Metastasizing to the Mandible, Including Molecular Analysis and a Review of the Literature. *Journal of Oral and Maxillofacial Surgery*, doi:10.1016/j.joms.2016.06.004.
- Harrisson, K., et al. (2016) Pleistocene divergence across a mountain range and the influence of selection on mitogenome evolution in threatened Australian freshwater cod species. *Heredity*. 1–10. doi:10.1038/hdy.2016.8.
- Hill, C. J. et al. (2016) Effect of room temperature transport vials on DNA quality and phylogenetic composition of faecal microbiota of elderly adults and infants. *Microbiome*. 4:19. doi: 10.1186/s40168-016-0164-3.
- Laver, T., Harrison, J., O'Neill, P. A., Moore, K., Farbos, A., Paszkiewicz, K. and Studholme, D. J. (2015) Assessing the performance of the Oxford Nanopore Technologies MinION. *Biomolecular Detection and Quantification* 3 (2015) 1–8. doi :10.1016/j.bdq.2015.02.001.
- Palomo, A., et al. (2016) Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of Nitrospira spp. *The ISME Journal*. doi:10.1038/ismej.2016.63.
- Shain, A. H., et al. (2015) The Genetic Evolution of Melanoma from Precursor Lesions. *The New England Journal of Medicine*. 373:1926-1936. doi: 10.1056/NEJMoa1502583.
- Tatarenkova, A., Mesaka F. and Avisea, J. C. (2015) Complete mitochondrial genome of a self-fertilizing fish *Kryptolebias marmoratus* (Cyprinodontiformes, Rivulidae) from Florida. *Mitochondrial DNA*. doi: 10.3109/19401736.2015.1115861.
- Yang, Y. A., et al. (2016) FOXA1 potentiates lineage-specific enhancer activation through modulating TET1 expression and function. *Nucleic Acids Research*. doi: 10.1093/nar/gkw498.